

Collaborators

The KBase collaboration is led by Lawrence Berkeley, Argonne, Brookhaven, and Oak Ridge national laboratories.

Also involved in the multi-institutional program are Cold Spring Harbor Laboratory; the University of California, Davis; Hope College; the University of Illinois at Urbana-Champaign; Yale University; and the University of Tennessee.

Our key external partners are the Joint Genome Institute, the Environmental Molecular Sciences Laboratory, and the Bioenergy Centers. Several university projects are also important contributors.

The Department of Energy Systems Biology Knowledgebase (KBase) is a new community resource for predictive biology. It integrates a wide spectrum of data types across the microbial, microbial community, and plant domains, and ties this data into a varied set of powerful computational tools that can analyze and simulate data to predict biological behavior, generate and test hypotheses, design new biological functions, and propose new experiments. The overarching objective is to provide a solid platform that supports predictive biology in a framework that does not require users to learn separate systems to formulate and answer questions spanning a variety of topics in systems biology research.

kbase.science.energy.gov

kbase.us

KBase is far more than just a database. It will allow researchers to quickly and easily map genotypes to molecular, organismal, and ecological phenotypes. KBase is an open-source and open-architecture integrated system that brings together diverse data and algorithms in a unified framework for prediction of biological structure and function with associated statistical confidence. It is also a development environment in which analysis tool developers are invited and trained to implement their new methods as KBase services, and biologists are encouraged to submit their datasets for community use. KBase is designed for continual update via both automated pipelines and user input and interaction. Our approach enables transparency and reproducibility in the complex, multidisciplinary workflows necessary for addressing biological problems in energy and the environment.



Please visit kbase.us/about for more information

Roadmap

Version 1.0 of KBase, available in early 2013, will offer a unified environment for users to view, query, and download data for microbes, plants, and microbial communities. Users will also be able to apply a series of powerful demonstration workflows, including genome annotation, metabolic modeling, and phenotype analysis.

Version 2.0 of KBase, available in late 2013, will include a narrative interface that provides an online environment for users to collaboratively piece together a wide variety of KBase tools and data into a scientific narrative. Additionally, the software will provide extensive support for integrated analysis of thousands of closely related genomes, including comparative analysis of metabolism, regulation, and model-predicted phenotypes.

Ultimately, KBase will provide a scalable framework for predictive biology and the effective socially-enabled development of biological information, methods, and conclusions. Integration across microbes, communities, and plants will enable the construction of models ranging from the genotypes of complex microbial and plant communities to their phenotypes, enabling researchers to optimize energy production and improve the environment.

Outreach

We are actively seeking collaborators, and are building a list of people to invite to our events. Our content and training topics are being guided by user feedback. Please contact us at outreach@kbase.us and we will set up a convenient time to speak with you. We are interested in collaborating with other large-scale bioinformatics projects and data generators, but also with investigators of projects spanning a range of scales.

Several types of training are being offered:

- Tutorials focused on using KBase
- Bootcamps focused on developing computational tools in KBase
- Workshops focused on scientific problems



We are maintaining a list of FAQs at kbase.us/about/general-faqs